

SEQUENCE LISTING

<110> Edwin L. Madison
Edgar O. Ong

<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

<140>

<141> Herewith

<150> 60/275,592

<151> 2001-03-13

<160> 22

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<213> Homo Sapien

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<221> CDS

<222> (23) . . . (2589)

<223> Nucleotide sequence encoding MTSP1

<300>

<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank #AR081724

<309> 2000-08-31

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<311> 1998-02-20

<312> 1999-10-26

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gag	aa	gt	aa	tt	gag	gaa	gg	gt	gag	tt	ct	cc	gt	aa		148
Glu	Lys	Val	Asn	Gly	Leu	Glu	Gly	Val	Glu	Phe	Leu	Pro	Val	Asn		
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aa	gt	aa	gt	gaa	aa	cat	gg	cc	gg	cg	tg	gt	gt	ct		196
Asn	Val	Lys	Val	Gly	Leu	Glu	Gly	Pro	Gly	Arg	Trp	Val	Val	Leu		
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gcg ctg aag ctg ctg tac agc gga gtc cca ttc ctg ggc ccc tac cac Ala Leu Lys Leu Tyr Ser Gly Val Pro Phe Leu Gly Pro Tyr His 125 130 135				436
aag gag tcg gct gtg acg gcc ttc agc gag ggc agc gtc atc gcc tac Lys Glu Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr 140 145 150				484
tac tgg tct gag ttc agc atc ccg cag cac ctg gtg gag gag gcc gag Tyr Trp Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu 155 160 165 170				532
cgc gtc atg gcc gag gag cgc gta gtc atg ctg ccc ccg cg gcg cgc Arg Val Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg 175 180 185				580
tcc ctg aag tcc ttt gtg gtc acc tca gtg gtg gct ttc ccc acg gac Ser Leu Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp 190 195 200				628
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cac gcc cgc ggt gtg gag ctg atg cgc ttc acc acg ccc ggc ttc cct His Ala Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro 220 225 230				724
gac agc ccc tac ccc gct cat gcc cgc tgc cag tgg gcc ctg cg gg Asp Ser Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly 235 240 245 250				772
gac gcc gac tca gtg ctg agc ctc acc ttc cgc agc ttt gac ctt gc Asp Ala Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala 255 260 265				820
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ccc tcc tac aac ctg acc ttc cac tcc tcc cag aac gtc ctg ctc atc Pro Ser Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile 300 305 310				964
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aac att gac tgc aca tgg aac att gag gtg ccc aac aac cag cat gtg Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val 365 370 375	1156
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gaa tac ctc tcc tac gac tcc agt gac cca tgc ccg ggg cag ttc acg Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr 445 450 455	1396
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gcc gac tgc acc gac cac agc gat gag ctc aac tgc agt tgc gac gcc Ala Asp Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala 475 480 485 490	1492
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acg gat gcg gat gag ggc gag tgg ccc tgg cag gta agc ctg cat gct Thr Asp Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala 620 625 630	1924
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ctg caa aag ggt gag atc cgc gtc atc aac cag acc acc tgc gag aac Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr Thr Cys Glu Asn 765 770 775	2356
ctc ctg ccg cag cag atc acg ccg cgc atg atg tgc gtg ggc ttc ctc Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys Val Gly Phe Leu 780 785 790	2404
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Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val Tyr Thr Arg Leu		
830	835	840
cct ctg ttt cgg gac tgg atc aaa gag aac act ggg gta ta gggccgggg		2599
Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly Val		
845	850	855
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ggctggagac tggaccgctg actgcaccag cgccccaga acatacactg tgaactcaat		2719
ctccaggct ccaaattctgc ctagaaaaacc tctcgcttcc tcagcctcca aagtggagct		2779
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35 40 45		
Lys His Gly Pro Gly Arg Trp Val Val Leu Ala Ala Val Leu Ile Gly		
50 55 60		
Leu Leu Leu Val Leu Leu Gly Ile Gly Phe Leu Val Trp His Leu Gln		
65 70 75 80		
Tyr Arg Asp Val Arg Val Gln Lys Val Phe Asn Gly Tyr Met Arg Ile		
85 90 95		
Thr Asn Glu Asn Phe Val Asp Ala Tyr Glu Asn Ser Asn Ser Thr Glu		
100 105 110		
Phe Val Ser Leu Ala Ser Lys Val Lys Asp Ala Leu Lys Leu Leu Tyr		
115 120 125		
Ser Gly Val Pro Phe Leu Gly Pro Tyr His Lys Glu Ser Ala Val Thr		
130 135 140		
Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp Ser Glu Phe Ser		
145 150 155 160		
Ile Pro Gln His Leu Val Glu Ala Glu Arg Val Met Ala Glu Glu		
165 170 175		
Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu Lys Ser Phe Val		
180 185 190		
Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys Thr Val Gln Arg		
195 200 205		
Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala Arg Gly Val Glu		
210 215 220		
Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser Pro Tyr Pro Ala		
225 230 235 240		
His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala Asp Ser Val Leu		
245 250 255		
Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys Asp Glu Arg Gly		

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275							280								285
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Phe	His	Ser	Ser	Gln	Asn	Val	Leu	Leu	Ile	Thr	Leu	Ile	Thr	Asn	Thr
305							310								320
Glu	Arg	Arg	His	Pro	Gly	Phe	Glu	Ala	Thr	Phe	Phe	Gln	Leu	Pro	Arg
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Met	Ser	Ser	Cys	Gly	Gly	Arg	Leu	Arg	Lys	Ala	Gln	Gly	Thr	Phe	Asn
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Ser	Pro	Tyr	Tyr	Pro	Gly	His	Tyr	Pro	Pro	Asn	Ile	Asp	Cys	Thr	Trp
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Asn	Ile	Glu	Val	Pro	Asn	Asn	Gln	His	Val	Lys	Val	Ser	Phe	Lys	Phe
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Phe	Tyr	Leu	Leu	Glu	Pro	Gly	Val	Pro	Ala	Gly	Thr	Cys	Pro	Lys	Asp
385							390								400
Tyr	Val	Glu	Ile	Asn	Gly	Glu	Lys	Tyr	Cys	Gly	Glu	Arg	Ser	Gln	Phe
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Val	Val	Thr	Ser	Asn	Ser	Asn	Lys	Ile	Thr	Val	Arg	Phe	His	Ser	Asp
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Gln	Ser	Tyr	Thr	Asp	Thr	Gly	Phe	Leu	Ala	Glu	Tyr	Leu	Ser	Tyr	Asp
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Ile	Arg	Lys	Glu	Leu	Arg	Cys	Asp	Gly	Trp	Ala	Asp	Cys	Thr	Asp	His
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Ser	Asp	Glu	Leu	Asn	Cys	Ser	Cys	Asp	Ala	Gly	His	Gln	Phe	Thr	Cys
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Lys	Asn	Lys	Phe	Cys	Lys	Pro	Leu	Phe	Trp	Val	Cys	Asp	Ser	Val	Asn
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Asp	Cys	Gly	Asp	Asn	Ser	Asp	Glu	Gln	Gly	Cys	Ser	Cys	Pro	Ala	Gln
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Thr	Phe	Arg	Cys	Ser	Asn	Gly	Lys	Cys	Leu	Ser	Lys	Ser	Gln	Gln	Cys
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Asn	Gly	Lys	Asp	Asp	Cys	Gly	Asp	Gly	Ser	Asp	Glu	Ala	Ser	Cys	Pro
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Gly	Leu	Cys	Leu	Ser	Lys	Gly	Asn	Pro	Glu	Cys	Asp	Gly	Lys	Glu	Asp
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Glu	Trp	Pro	Trp	Gln	Val	Ser	Leu	His	Ala	Leu	Gly	Gln	Gly	His	Ile
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Cys	Gly	Ala	Ser	Leu	Ile	Ser	Pro	Asn	Trp	Leu	Val	Ser	Ala	Ala	His
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Val	Gln	Glu	Arg	Arg	Leu	Lys	Arg	Ile	Ile	Ser	His	Pro	Phe	Phe	Asn
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Asp	Phe	Thr	Phe	Asp	Tyr	Asp	Ile	Ala	Leu	Leu	Glu	Leu	Glu	Lys	Pro
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His	Val	Phe	Pro	Ala	Gly	Lys	Ala	Ile	Trp	Val	Thr	Gly	Trp	Gly	His
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 Thr Pro Arg Met Met Cys Val Gly Phe Leu Ser Gly Gly Val Asp Ser
 785 790 795 800
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Ser Ser Val Glu Ala Asp Gly
 805 810 815
 Arg Ile Phe Gln Ala Gly Val Val Ser Trp Gly Asp Gly Cys Ala Gln
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<220>
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His Asp Gln Ser Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu	
65 70 75 80	
Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr	
85 90 95	
Asp Ile Ala Leu Leu Glu Leu Glu Lys Pro Ala Glu Tyr Ser Ser Met	
100 105 110	
Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly	
115 120 125	
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr	
130 135 140	
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr	
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Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys	
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Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly	
195 200 205	
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val	
210 215 220	
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly	
225 230 235 240	
Val	

<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
aatggccatg gcaggccagc ctcc

24

<210> 6

24745-1613

<211> 32
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<220>
<223> Primer

<400> 6 32
gtcccaaact tactataacct acaatgtacc ag

<210> 7
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 7 32
gtccccaaact tactataacct acaatgtacc ag

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 8 24
aatggccatg gcaggccagc ctcc

<210> 9
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 9 31
tgccattacc agcatcctct tctactcaaa g

<210> 10
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 10 33
ccatgtgtat aactcacgga caatccacac tac

<210> 11
<211> 10
<212> PRT
<213> Homo sapien

<400> 11
Met Pro Leu Pro Ala Ser Ser Ser Thr Gln

24745-1613

24745-1613

<210> 16
<211> 438
<212> PRT
<213> Homo sapien

<400> 16
 Met Met Tyr Thr Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala
 1 5 10 15
 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
 20 25 30
 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
 85 90 95
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
 100 105 110
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
 115 120 125
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
 130 135 140
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
 145 150 155 160
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
 165 170 175
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
 180 185 190
 Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln
 195 200 205
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 210 215 220
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
 225 230 235 240
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
 245 250 255
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
 260 265 270 275
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
 275 280 285
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
 290 295 300
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
 305 310 315 320
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
 325 330 335
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
 340 345 350
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
 355 360 365
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
 370 375 380
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
 385 390 395 400
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
 405 410 415
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
 420 425 430
 Ala Ser Lys Thr Gly Met
 435

<210> 17
<211> 702
<212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1) ... (702)

<223> Nucleotide sequence encoding Protease Domain

<400> 17		
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Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln		
1 5 10 15		
gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc		96
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu		
20 25 30		
atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat		144
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn		
35 40 45		
aaa gac cca actcaa tgg att gct act ttt ggt gca act ata aca cca		192
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro		
50 55 60		
ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac		240
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr		
65 70 75 80		
cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act		288
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr		
85 90 95		
gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca		336
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser		
100 105 110		
tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga		384
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly		
115 120 125		
tcc att gta gat gat gga cct ata caa aat aca ctt cggt caa gcc aga		432
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg		
130 135 140		
gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat		480
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp		
145 150 155 160		
ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa		528
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys		
165 170 175		
ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat		576
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn		
180 185 190		
cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt		624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys		
195 200 205		
gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga		672

Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220

gat tgg att gcc tca aag act ggt atg tag
 Asp Trp Ile Ala Ser Lys Thr Gly Met *
 225 230

702

<210> 18
 <211> 233
 <212> PRT
 <213> Homo sapien

<400> 18
 Ile Val Gln Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln
 1 5 10 15
 Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu
 20 25 30
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
 85 90 95
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
 100 105 110
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
 115 120 125
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
 130 135 140
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
 145 150 155 160
 Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
 165 170 175
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
 180 185 190
 His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
 195 200 205
 Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220
 Asp Trp Ile Ala Ser Lys Thr Gly Met
 225 230

<210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg

42

<210> 20
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Primer

<400> 20
agatgaggct gggaggctaa ctctctggac tat 33

<210> 21
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 21
attcgccggcc gcctacatac cagtcttga ggcaat 35

<210> 22
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 22
atagtccaga gagtttagcct cccagactca tct 33